(1) GENERAL INFORMATION:
    (i) APPLICANT: Simons, Michael
              Volk, Rudiger
              Horowitz, Arie
    (ii) TITLE OF INVENTION: Stimulation of angiogenesis
via enhanced endothelial expression of syndecan-4
core proteins
    (iii) NUMBER OF SEQUENCES: 16
    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: David Prashker, Esq.
        (B) STREET: P.O. Box 5387
        (C) CITY: Magnolia
        (D) STATE: Massachusetts
        (E) COUNTRY: USA
        (F) ZIP: 01930
    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
        (B) COMPUTER: IBM PS/1
        (C) OPERATING SYSTEM: MS DOS
        (D) SOFTWARE: WordPerfect version 5.1
    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: 09/145,916
        (B) FILING DATE: September 2, 1998
        (C) CLASSIFICATION: Unknown
    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: David Prashker, Esq.
        (B) REGISTRATION NUMBER: 29,693
        (C) REFERENCE/DOCKET NUMBER: BIS-039
    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (978) 525-3794
(2) INFORMATION FOR SEQ ID NO:1:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 762 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGCGCGCTGG CGCTGCGCCT GCAGCCTGCC  60
CTCCCGCAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC  120
TCAGACAACT TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG  180
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC  240
ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG  300
GAGGGAGAGC CCGTGGCCCA CGTGGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG  360
AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA  420
ACAGCAGCCA GAGCCACCAC GGCCCAGGCA TCTGTCACGT CTCATCCCCA CGGGGATGTG  480
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT  540
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAGAGG TTGTGGAGGA TGAAACTACC  600
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG  660
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA  720
GGAGCCACAG GTGCTTCTCA GGGCCTTTTG GACAGGAAGG AA                      762
```

(2) INFORMATION FOR SEQ ID NO:2:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1020 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG  60
GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC  120
GCTGCTCTCC AGATACCCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCCGCTCTG  180
CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCTT AAAACCAGAA  240
```

```
ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
AGTGAGAGGG CGCCGCGTTC CCGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
AGGAAGCGAG CGCCCCGAG CCCCGAGCCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
GGTACTCTGC TCCGGATTCG TGTGCGCGGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540
TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT GCGGCGCGCG 600
TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCGTGTCGG CGGAGTCGAG AGCAGAGCTG 660
ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTTGACTAG TGCTGCTCCA 840
AAAGTGGAAA CCACGACGCT GAATATACAG AACAAGATAC CTGCTCAGAC AAAGTCACCT 900
GAAGAAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020
```

(2) INFORMATION FOR SEQ ID NO:3:
  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 340 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Glu Lys Glu Glu
1               5                   10                  15
Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
                20                  25                  30
Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
                35                  40                  45
Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
            50                  55                  60
Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
65                  70                  75                  80
Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
                85                  90                  95
Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
                100                 105                 110
Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
            115                 120                 125
Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
        130                 135                 140
Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
145                 150                 155                 160
Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
                165                 170                 175
Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
                180                 185                 190
Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
            195                 200                 205
Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
    210                 215                 220
Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
225                 230                 235                 240
Pro Ile Asp Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
                245                 250                 255
Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
                260                 265                 270
Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
            275                 280                 285
Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
        290                 295                 300
Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
305                 310                 315                 320
Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
                325                 330                 335
```

Lys Arg Thr Glu
             340

(2) INFORMATION FOR SEQ ID NO:4:
        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1079 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCGCGGAG CTGCGGCGCC 60
TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
TGGAGACAGC GGTCAGCCTC ACCACGGACA CGTCCGTCCC ACTGCCCACC ACGGTGGCCG 300
TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGCACCA 540
CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCCT GCCCCCCTTT GTCACCAAGG 600
CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCCACCAC CTCCATCCCT GAAACCAGTG 660
TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCCACGGA AAAAAGCACT GCCTTGCCTT 780
CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
CACCACCAGC AGCACCGGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

(2) INFORMATION FOR SEQ ID NO:5:
        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 447 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG TCTGCCTGTT TGCGCCGGTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
GCCCCAGGCG AGTCGATTCG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCTTGA GCAGGACTCT 180
GACTTTGAGC TGTCGGGTTC CGGAGATCTA GATGACACGG AGGAGCCCAG GACCTTCCCT 240
GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300
ATCCGTGTCC CCTCAGAGCC CAAGGAACTG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
GGCAGCAACA TTTTTGAAAG AACTGAG 447

(2) INFORMATION FOR SEQ ID NO:6:
        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 1590 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGACATGG AGGAGAACCT GGCCAACCAC 240
AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGGGCC TGCTGAATGA CTCGGAGCGT 360
ACACTGCAGG ATGCTTTTCC CGGGGCCTTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540

```
CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCACTGCGG 600
CCGTTTGGGG ATGCCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
CGATCCTTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCCAGGTT 720
CCTCTGGCCC CAGAATGTTC TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
GGAGTCCCTG GTGCCCGGGC CTGTCCCGAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAGGACA CACTCACAGC TAAGGTCATC 1020
CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
GAGGCCAAGG CCCAGCTCCG AGACATTCAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
TGTAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTCC 1260
AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCCT 1320
GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCCT TGACCCATGC CCTCCCCGGC 1560
TTGTCAGAAC AGGAGGGACA GAAGACCTCG                              1590
```

(2) INFORMATION FOR SEQ ID NO:7:
     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 531 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
1               5               10                  15
Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
                20              25                  30
Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
            35              40                  45
Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
        50              55                  60
Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
65              70                  75                      80
Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu
                85              90                  95
Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
            100             105                 110
Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly
        115                 120                 125
Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
        130             135                 140
Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu
145             150                 155                 160
Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
                165                 170                 175
Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu
            180                 185                 190
Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu
            195                 200                 205
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val
        210                 215                 220
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val
225                 230                 235                 240
Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys
                245                 250                 255
Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys
            260                 265                 270
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala
            275                 280                 285
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe
```

```
            290                  295                  300
Trp Gly Pro Ser Gly Ala Glu Asn Val Ile Gly Ser Val His Met Trp
305                  310                  315                  320
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr
                325                  330                  335
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro His Gly
            340                  345                  350
Ser Gly Pro Glu Glu Lys Arg Arg Arg Gly Lys Leu Ala Leu Gln Glu
            355                  360                  365
Lys Ser Ser Thr Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala
            370                  375                  380
Gln Leu Arg Asp Ile Gln Asp Tyr Trp Ile Ser Leu Pro Gly Thr Leu
385                  390                  395                  400
Cys Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp Asp Arg Cys Trp
                405                  410                  415
Asn Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly
                420                  425                  430
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys
                435                  440                  445
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr
            450                  455                  460
Asn Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp
465                  470                  475                  480
Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Gly Gly Cys Pro Asp
                485                  490                  495
Asp Ala Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Ser Arg Thr
            500                  505                  510
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys
            515                  520                  525
Thr Ser Ala
530
```

(2) INFORMATION FOR SEQ ID NO:8:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 75 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
GTGCTGGGAG GTGTCATTGC TGGAGGCCTG GTGGGCCTCA TCTTTGCTGT GTGCCTGGTG 60
GCTTTCATGC TATAC                                                 75
```

(2) INFORMATION FOR SEQ ID NO:9:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 72 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTTC TCTTTGCAAT TTTTCTTATC 60
CTGCTGTTGG TG                                                    72
```

(2) INFORMATION FOR SEQ ID NO:10:
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 24 amino acids
                (B) TYPE: amino acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala
1                   5                   10                  15
```

```
Ile Phe Leu Ile Leu Leu Leu Val
          20


(2) INFORMATION FOR SEQ ID NO:11:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 75 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:


GTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTTGCTGC CTTCCTTGTC 60
ATGCTGCTCA TCTAC                                                  75


(2) INFORMATION FOR SEQ ID NO:12:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 75 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:


GTCTTGGCAG CTCTGATTGT GGGCGGCGTA GTGGGCATCC TCTTCGCCGT TTTCCTGATC 60
CTGCTGCTGG TGTAC                                                  75


(2) INFORMATION FOR SEQ ID NO:13:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 93 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:


GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTCAC CTTGGTCCTT 60
GCTGCAGCCA GGCCCAGGTG GCGGTAACTG CCC                              93


(2) INFORMATION FOR SEQ ID NO:14:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 27 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:


Ala Thr Arg Pro Glu Pro His Tyr Phe Phe Leu Leu Phe Leu Phe Thr
1               5                   10                  15
Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg
          20                  25


(2) INFORMATION FOR SEQ ID NO:15:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 83 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:


TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60
CCACCAGCCC TGCAGGCACT GCC                                         83


(2) INFORMATION FOR SEQ ID NO:16:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 87 base pairs
            (B) TYPE: nucleic acid
```

```
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60
GCCCCCACCA ACGAGTTCTA CGCATGA                                   87
```